**Page 21, line 16, paragraph 12**: Please amend as follows:

Figs. 36A-36F: Functional map and sequence of the β-lactamase cassette for replacement of CDRs for CDR library cloning.

**Page 21, line 18, paragraph 13**: Please amend as follows:

Figs. 37A-37D: Oligo and primer design for Vκ CDR3 libraries.

B4

**Page 21, line 19, paragraph 14**: Please amend as follows:

Figs. 38A-38D: Oligo and primer design for Vλ CDR3 libraries.

**Page 21, line 21, paragraph 16**: Please amend as follows:

B5

Figs. 40A-40B: Expression of all 49 HuCAL scFvs obtained by combining each of the 7 VH genes with each of the 7 VL genes (pBS 13, 30 °C): Values are given for the percentage of soluble vs. insoluble material, the total and the soluble amount compared to the combination H3P2, which was set to 100%. In addition, the corresponding values for the McPC603 scFv are given.

## REMARKS

By the foregoing, the "Brief Description of the Drawings" section of the specification is rendered consistent with the formal drawings filed concurrently herewith. A copy of the "Brief Description of the Drawings" showing the amendments with brackets and underlining is attached.

Respectfully submitted,

March 29, 2001
Date

for Reg. No. 33,715
Colin G. Sandercock
Reg. No. 31,298

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**Amendments to specification with brackets and underlining**

**Page 18, line 4, paragraph 2**: Please amend as follows:

[Fig. 2] Figs. 2A-2G: Alignment of consensus sequences designed for each subgroup (amino acid residues are shown with their standard one-letter abbreviation). [(A)] (2A-2B) kappa sequences, [(B)] (2C-2D) lambda sequences and [(C)] (2E-2G), heavy chain sequences. The positions are numbered according to Kabat (1991). In order to maximize homology in the alignment, gaps (-) have been introduced in the sequence at certain positions.

**Page 18, line 10, paragraph 3**: Please amend as follows:

[Fig. 3] Figs. 3A-3K: Gene sequences of the synthetic V kappa consensus genes. The corresponding amino acid sequences (see [Fig. 2] Figs. 2A-2B) as well as the unique cleavage sites are also shown.

**Page 18, line 13, paragraph 4**: Please amend as follows:

[Fig. 4] Figs. 4A-4I: Gene sequences of the synthetic V lambda consensus genes. The corresponding amino acid sequences (see [Fig. 2] Figs. 2C-2D) as well as the unique cleavage sites are also shown.

**Page 18, line 16, paragraph 5**: Please amend as follows:

[Fig. 5] Figs. 5A-5U: Gene sequences of the synthetic V heavy chain consensus genes. The corresponding amino acid sequences (see [Fig. 2] Figs. 2E-2G) as well as the unique cleavage sites are also shown.

**Page 18, line 19, paragraph 6**: Please amend as follows:

[Fig. 6] Figs. 6A-6G: Oligonucleotides used for construction of the consensus genes. The oligos are named according to the corresponding consensus gene, e.g. the gene Vκ1 was constructed using the six oligonucleotides O1K1 to O1K6. The oligonucleotides used for synthesizing the genes encoding the constant domains Cκ (OCLK1 to 8) and CH1 (OCH1 to 8) are also shown.

**Page 18, line 25, paragraph 7**: Please amend as follows:

[Fig. 7A/B] Figs. 7A-7D: Sequences of the synthetic genes encoding the constant domains Cκ [(A)] (7A-7B) and CH1 [(B)] (7C-7D). The corresponding amino acid sequences as well as unique cleavage sites introduced in these genes are also shown.

**Page 18, line 28, paragraph 8**: Please amend as follows:

[Fig. 7C] Figs. 7E-7H: Functional map and sequence of module M24 comprising the synthetic Cλ gene segment (huCL lambda).

**Page 18, line 30, paragraph 9**: Please amend as follows:

[Fig. 7D] Figs. 7I-7J: Oligonucleotides used for synthesis of module M24.

**Page 18, line 31, paragraph 10**: Please amend as follows:

[Fig. 8] Figs. 8A-8E: Sequence and restriction map of the synthetic gene encoding the consensus single-chain fragment VH3-Vκ2. The signal sequence (amino acids 1 to 21) was derived from the *E. coli* phoA gene (Skerra & Plückthun, 1988). Between the phoA signal sequence and the VH3 domain, a short sequence stretch

encoding 4 amino acid residues (amino acid 22 to 25) has been inserted in order to allow detection of the single-chain fragment in Western blot or ELISA using the monoclonal antibody M1 (Knappik & Plückthun, 1994). The last 6 basepairs of the sequence were introduced for cloning purposes (EcoRI site).

**Page 19, line 14, paragraph 3**: Please amend as follows:

[Fig. 10] Figs. 10A-10B: Sequencing results of independent clones from the initial library, translated into the corresponding amino acid sequences. (A) Amino acid sequence of the VH3 consensus heavy chain CDR3 (position 93 to 102, Kabat numbering). (B) Amino acid sequences of 12 clones of the 10-mer library. (C) Amino acid sequences of 11 clones of the 15-mer library, *: single base deletion.

**Page 20, line 35, paragraph 10**: Please amend as follows:

[Fig. 25] Fig. 25A: Schematic representation of the modular pCAL vector system.

**Page 20, line 36, paragraph 11**: Please amend as follows:

[Fig. 25a] Figs. 25B-25C: List of restriction sites already used in or suitable for the modular HuCAL genes and pCAL vector system.

**Page 20, line 38, paragraph 12**: Please amend as follows:

[Fig. 26] Figs. 26A-26D: List of the modular vector elements for the pCAL vector series: shown are only those restriction sites which are part of the modular system.

**Page 21, line 1, paragraph 1**: Please amend as follows:

[Fig. 27] Figs. 27A-27B: Functional map and sequence of the multi-cloning site module (MCS).

**Page 21, line 2, paragraph 2**: Please amend as follows:

[Fig. 28] Figs. 28A-28G: Functional map and sequence of the pMCS cloning vector series.

**Page 21, line 3, paragraph 3**: Please amend as follows:

[Fig. 29] Figs. 29A-29B: Functional map and sequence of the pCAL module M1 (see [Fig. 26] Figs. 26A-26D).

**Page 21, line 4, paragraph 4**: Please amend as follows:

[Fig. 30] Figs. 30A-30C: Functional map and sequence of the pCAL module M7-III (see [Fig. 26] Figs. 26A-26D).

**Page 21, line 5, paragraph 5**: Please amend as follows:

[Fig. 31] Figs. 31A-31B: Functional map and sequence of the pCAL module M9-II (see [Fig. 26] Figs. 26A-26D).

**Page 21, line 6, paragraph 6**: Please amend as follows:

[Fig. 32] Figs. 32A-32C: Functional map and sequence of the pCAL module M11-II (see [Fig. 26] Figs. 26A-26D).

**Page 21, line 7, paragraph 7**: Please amend as follows:

[Fig. 33] Figs. 33A-33D: Functional map and sequence of the pCAL module M14-Ext2 (see [Fig. 26] Figs. 26A-26D).

**Page 21, line 9, paragraph 8**: Please amend as follows:

[Fig. 34] Figs. 34A-34D: Functional map and sequence of the pCAL module M17 (see [Fig. 26] Figs. 26A-26D).

**Page 21, line 10, paragraph 9**: Please amend as follows:

[Fig. 35] Figs. 35A-35I: Functional map and sequence module vector pCAL4.

**Page 21, line 11, paragraph 10**: Please amend as follows:

[Fig. 35a] Figs. 35J-35XXX: Functional maps and sequences of additional pCAL modules (M2, M3, M7I, M7II, M8, M10II, M11II, M12, M13, M19, M20, M21, M41) and of low-copy number plasmid vectors (pCALO1 to pCALO3).

**Page 21, line 14, paragraph 11**: Please amend as follows:

[Fig. 35b] Figs. 35YYY-35CCCC: List of oligonucleotides and primers used for synthesis of pCAL vector modules.

**Page 21, line 16, paragraph 12**: Please amend as follows:

[Fig. 36] Figs. 36A-36F: Functional map and sequence of the β-lactamase cassette for replacement of CDRs for CDR library cloning.

**Page 21, line 18, paragraph 13**: Please amend as follows:

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[Fig. 40] Figs. 40A-40B: Expression of all 49 HuCAL scFvs obtained by combining each of the 7 VH genes with each of the 7 VL genes (pBS 13, 30 °C): Values are given for the percentage of soluble vs. insoluble material, the total and the soluble amount compared to the combination H3P2, which was set to 100%. In addition, the corresponding values for the McPC603 scFv are given.